BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/050,888_

Source: _OIPE_

Date Processed by STIC: _2/6/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , EFS Submission User Manual - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
    U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
            Or
    U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/050,888

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics
     Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
     Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length

Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
     "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences
     (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
     (NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
     (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

No

10_____Invalid <213>
     Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
     "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING   DATE: 02/06/2002
PATENT APPLICATION: US/10/050,888   TIME: 07:28:41

     Input Set : **A:\Seqlist.txt**
     Output Set: **N:\CRF3\02062002\J050888.raw**

rr 1-3

Does Not Comply
Corrected Diskette Needed

```
 3 <110> APPLICANT: Gesteland, Raymond F.
 4        Giddings, Michael C.
 5        Matveeva, Olga V.
 6        Atkins, John F.
 8 <120> TITLE OF INVENTION: Finding Active Antisense Oligonucleotides Using
 9        Artificial Neural Networks
11 <130> FILE REFERENCE: T9479.B
13 <140> CURRENT APPLICATION NUMBER: US/10/050,888
15 <141> CURRENT FILING DATE: 2002-01-14
17 <150> PRIOR APPLICATION NUMBER: US 60/262,993
19 <151> PRIOR FILING DATE: 2001-01-19
21 <160> NUMBER OF SEQ ID NOS: 20
23 <210> SEQ ID NO: 1
25 <211> LENGTH: 21
27 <212> TYPE: DNA
29 <213> ORGANISM:
31 <400> SEQUENCE: 1
33 cctctttccc ttaccctcct g 21
35 <210> SEQ ID NO: 2
37 <211> LENGTH: 20
39 <212> TYPE: DNA
41 <213> ORGANISM:
43 <400> SEQUENCE: 2
45 gtcagccatg gtcccccccc 20
47 <210> SEQ ID NO: 3
49 <211> LENGTH: 21
51 <212> TYPE: DNA
53 <213> ORGANISM:
55 <400> SEQUENCE: 3
57 cttgagctca gctccctcag g 21
59 <210> SEQ ID NO: 4
61 <211> LENGTH: 21
63 <212> TYPE: DNA
65 <213> ORGANISM:
67 <400> SEQUENCE: 4
69 cctattccct ttcctcccaa a 21
71 <210> SEQ ID NO: 5
73 <211> LENGTH: 21
75 <212> TYPE: DNA
77 <213> ORGANISM:
79 <400> SEQUENCE: 5
81 tccactcccc cgatccactc a 21
83 <210> SEQ ID NO: 6
```

W--> (lines 29, 41, 53, 65, 77)

→ mandatory numeric identifier and response needed

(global erra)

(see item 10 on Erra Summary sheet)

```
         85 <211> LENGTH: 21
         87 <212> TYPE: DNA
W-->   89 <213> ORGANISM:
         91 <400> SEQUENCE: 6
         93 aacccttatt tgtgtcccac c 21
         95 <210> SEQ ID NO: 7
         97 <211> LENGTH: 20
         99 <212> TYPE: DNA
W-->  101 <213> ORGANISM:
        103 <400> SEQUENCE: 7
        106 cccccaccac ttcccctctc 20
        108 <210> SEQ ID NO: 8
        110 <211> LENGTH: 20
        112 <212> TYPE: DNA
W-->  114 <213> ORGANISM:
        116 <400> SEQUENCE: 8
        118 cggtcccctt caagatccat 20
        120 <210> SEQ ID NO: 9
        122 <211> LENGTH: 20
        124 <212> TYPE: DNA
W-->  126 <213> ORGANISM:
        128 <400> SEQUENCE: 9
        130 tgcttaccct cccacagcag 20
        132 <210> SEQ ID NO: 10
        134 <211> LENGTH: 21
        136 <212> TYPE: DNA
W-->  138 <213> ORGANISM:
        140 <400> SEQUENCE: 10
        142 agagccacaa ttccctttct a 21
        144 <210> SEQ ID NO: 11
        146 <211> LENGTH: 14
        148 <212> TYPE: DNA
W-->  150 <213> ORGANISM:
        152 <400> SEQUENCE: 11
        154 cgaggccacc actc 14
        156 <210> SEQ ID NO: 12
        158 <211> LENGTH: 15
        160 <212> TYPE: DNA
W-->  162 <213> ORGANISM:
        164 <400> SEQUENCE: 12
        166 ccaccactca tctcg 15
        168 <210> SEQ ID NO: 13
        170 <211> LENGTH: 21
        172 <212> TYPE: DNA
W-->  174 <213> ORGANISM:
        176 <400> SEQUENCE: 13
        178 cccccaccac ttcccctctc a 21
        180 <210> SEQ ID NO: 14
        182 <211> LENGTH: 20
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RAW SEQUENCE LISTING   DATE: 02/06/2002
PATENT APPLICATION: US/10/050,888   TIME: 07:28:41

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\02062002\J050888.raw

```
        184 <212> TYPE: DNA
W-->    186 <213> ORGANISM:
        188 <400> SEQUENCE: 14
        190 cattccatga actctgcaag 20
        192 <210> SEQ ID NO: 15
        194 <211> LENGTH: 21
        196 <212> TYPE: DNA
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        200 <400> SEQUENCE: 15
        202 cccttaggtt tcccagcaag c 21
        204 <210> SEQ ID NO: 16
        206 <211> LENGTH: 15
        208 <212> TYPE: DNA
W-->    210 <213> ORGANISM:
        212 <400> SEQUENCE: 16
        214 tttgtgtccc acctg 15
        216 <210> SEQ ID NO: 17
        218 <211> LENGTH: 21
        220 <212> TYPE: DNA
W-->    222 <213> ORGANISM:
        224 <400> SEQUENCE: 17
        226 tgatccactc cccctccac t 21
        228 <210> SEQ ID NO: 18
        230 <211> LENGTH: 20
        232 <212> TYPE: DNA
W-->    234 <213> ORGANISM:
        236 <400> SEQUENCE: 18
        238 tgccagtcca catagtgttt 20
        240 <210> SEQ ID NO: 19
        242 <211> LENGTH: 21
        244 <212> TYPE: DNA
W-->    246 <213> ORGANISM:
        248 <400> SEQUENCE: 19
        250 tgatccactc cccctccac t 21
        252 <210> SEQ ID NO: 20
        254 <211> LENGTH: 20
        256 <212> TYPE: DNA
W-->    258 <213> ORGANISM:
        260 <400> SEQUENCE: 20
        262 aacccagtgc tccctttgct 20
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VERIFICATION SUMMARY   DATE: 02/06/2002
PATENT APPLICATION: US/10/050,888   TIME: 07:28:42

Input Set : **A:\Seqlist.txt**
Output Set: **N:\CRF3\02062002\J050888.raw**

```
L:13  M:270 C: Current Application Number differs, Replaced Application Number
L:15  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:29  M:201 W: Mandatory field data missing, <213> ORGANISM
L:41  M:201 W: Mandatory field data missing, <213> ORGANISM
L:53  M:201 W: Mandatory field data missing, <213> ORGANISM
L:65  M:201 W: Mandatory field data missing, <213> ORGANISM
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L:89  M:201 W: Mandatory field data missing, <213> ORGANISM
L:101 M:201 W: Mandatory field data missing, <213> ORGANISM
L:114 M:201 W: Mandatory field data missing, <213> ORGANISM
L:126 M:201 W: Mandatory field data missing, <213> ORGANISM
L:138 M:201 W: Mandatory field data missing, <213> ORGANISM
L:150 M:201 W: Mandatory field data missing, <213> ORGANISM
L:162 M:201 W: Mandatory field data missing, <213> ORGANISM
L:174 M:201 W: Mandatory field data missing, <213> ORGANISM
L:186 M:201 W: Mandatory field data missing, <213> ORGANISM
L:198 M:201 W: Mandatory field data missing, <213> ORGANISM
L:210 M:201 W: Mandatory field data missing, <213> ORGANISM
L:222 M:201 W: Mandatory field data missing, <213> ORGANISM
L:234 M:201 W: Mandatory field data missing, <213> ORGANISM
L:246 M:201 W: Mandatory field data missing, <213> ORGANISM
L:258 M:201 W: Mandatory field data missing, <213> ORGANISM
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